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09/807345 #3

SEQUENCE LISTING

<110> ARKHAMMA, Per C. et al.

<120> AN IMPROVED METHOD FOR EXTRACTING QUANTITATIVE INFORMATION RELATING TO AN INFLUENCE ON A CELLULAR RESPONSE

<130> 0459-0571P

<140> 09/807,345

<141> 2001-04-12

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<170> PatentIn version 3.1

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<213> Aequorea victoria and mouse

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PatentIn version 3.1

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Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
225 230 235 240

Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Thr Met Ala Ala Ala
245 250 255

Ala Ala Gln Gly Gly Gly Gly Gly Glu Pro Arg Arg Thr Glu Gly Val
260 265 270

Gly Pro Gly Val Pro Gly Glu Val Glu Met Val Lys Gly Gln Pro Phe
275 280 285

Asp Val Gly Pro Arg Tyr Thr Gln Leu Gln Tyr Ile Gly Glu Gly Ala
290 295 300

Tyr Gly Met Val Ser Ser Ala Tyr Asp His Val Arg Lys Thr Arg Val
305 310 315 320

Ala Ile Lys Lys Ile Ser Pro Phe Glu His Gln Thr Tyr Cys Gln Arg
325 330 335

Thr Leu Arg Glu Ile Gln Ile Leu Leu Arg Phe Arg His Glu Asn Val
340 345 350

Ile Gly Ile Arg Asp Ile Leu Arg Ala Ser Thr Leu Glu Ala Met Arg
355 360 365

Asp Val Tyr Ile Val Gln Asp Leu Met Glu Thr Asp Leu Tyr Lys Leu
370 375 380

Leu Lys Ser Gln Gln Leu Ser Asn Asp His Ile Cys Tyr Phe Leu Tyr
385 390 395 400

Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asn Val Leu His
405 410 415

Arg Asp Leu Lys Pro Ser Asn Leu Leu Ser Asn Thr Thr Cys Asp Leu
420 425 430

Lys Ile Cys Asp Phe Gly Leu Ala Arg Ile Ala Asp Pro Glu His Asp
435 440 445

His Thr Gly Phe Leu Thr Glu Tyr Val Ala Thr Arg Trp Tyr Arg Ala
450 455 460

Pro Glu Ile Met Leu Asn Ser Lys Gly Tyr Thr Lys Ser Ile Asp Ile
465 470 475 480

Trp Ser Val Gly Cys Ile Leu Ala Glu Met Leu Ser Asn Arg Pro Ile
485 490 495

Phe Pro Gly Lys His Tyr Leu Asp Gln Leu Asn His Ile Leu Gly Ile
500 505 510

Leu Gly Ser Pro Ser Gln Glu Asp Leu Asn Cys Ile Ile Asn Met Lys
515 520 525

Ala Arg Asn Tyr Leu Gln Ser Leu Pro Ser Lys Thr Lys Val Ala Trp
530 535 540

Ala Lys Leu Phe Pro Lys Ser Asp Ser Lys Ala Leu Asp Leu Leu Asp
545 550 555 560

Arg Met Leu Thr Phe Asn Pro Asn Lys Arg Ile Thr Val Glu Glu Ala
565 570 575

Leu Ala His Pro Tyr Leu Glu Gln Tyr Tyr Asp Pro Thr Asp Glu Pro
580 585 590

Val Ala Glu Glu Pro Phe Thr Phe Ala Met Glu Leu Asp Asp Leu Pro
595 600 605

Lys Glu Arg Leu Lys Glu Leu Ile Phe Gln Glu Thr Ala Arg Phe Gln
610 615 620

Pro Gly Val Leu Glu Ala Pro
625 630

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<213> Aequorea victoria and human

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Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
1				5					10					15		
gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	96
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
			20					25					30			
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
			35				40					45				
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
	50					55					60					
ctg	acc	tac	ggc	gtg	cag	tgc	ttc	agc	cgc	tac	ccc	gac	cac	atg	aag	240
Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	
65					70				75					80		
cag	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
				85					90					95		
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
			100					105					110			
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
			115				120					125				
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
	130					135					140					
aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	480
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
145					150					155					160	
ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc	528
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
				165				170					175			
gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac	ggc	576
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	
			180					185					190			
ccc	gtg	ctg	ctg	ccc	gac	aac	cac	tac	ctg	agc	acc	cag	tcc	gcc	ctg	624
Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	
			195				200					205				
agc	aaa	gac	ccc	aac	gag	aag	cgc	gat	cac	atg	gtc	ctg	ctg	gag	ttc	672
Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	
	210					215					220					

act cac tcc att cca gaa aac act aac ttc cca gca gga att gag cca	1392
Thr His Ser Ile Pro Glu Asn Thr Asn Phe Pro Ala Gly Ile Glu Pro	
450 455 460	
cag agt aat tat att cca gaa acg cca cct cct gga tat atc agt gaa	1440
Gln Ser Asn Tyr Ile Pro Glu Thr Pro Pro Pro Gly Tyr Ile Ser Glu	
465 470 475 480	
gat gga gaa aca agt gac caa cag ttg aat caa agt atg gac aca ggc	1488
Asp Gly Glu Thr Ser Asp Gln Gln Leu Asn Gln Ser Met Asp Thr Gly	
485 490 495	
tct cca gca gaa cta tct cct act act ctt tcc cct gtt aat cat agc	1536
Ser Pro Ala Glu Leu Ser Pro Thr Thr Leu Ser Pro Val Asn His Ser	
500 505 510	
ttg gat tta cag cca gtt act tac tca gaa cct gca ttt tgg tgt tca	1584
Leu Asp Leu Gln Pro Val Thr Tyr Ser Glu Pro Ala Phe Trp Cys Ser	
515 520 525	
ata gca tat tat gaa tta aat cag agg gtt gga gaa acc ttc cat gca	1632
Ile Ala Tyr Tyr Glu Leu Asn Gln Arg Val Gly Glu Thr Phe His Ala	
530 535 540	
tca cag ccc tca ctc act gta gat ggc ttt aca gac cca tca aat tca	1680
Ser Gln Pro Ser Leu Thr Val Asp Gly Phe Thr Asp Pro Ser Asn Ser	
545 550 555 560	
gag agg ttc tgc tta ggt tta ctc tcc aat gtt aac cga aat gcc acg	1728
Glu Arg Phe Cys Leu Gly Leu Leu Ser Asn Val Asn Arg Asn Ala Thr	
565 570 575	
gta gaa atg aca aga agg cat ata gga aga gga gtg cgc tta tac tac	1776
Val Glu Met Thr Arg Arg His Ile Gly Arg Gly Val Arg Leu Tyr Tyr	
580 585 590	
ata ggt ggg gaa gtt ttt gct gag tgc cta agt gat agt gca atc ttt	1824
Ile Gly Gly Glu Val Phe Ala Glu Cys Leu Ser Asp Ser Ala Ile Phe	
595 600 605	
gtg cag agc ccc aat tgt aat cag aga tat ggc tgg cac cct gca aca	1872
Val Gln Ser Pro Asn Cys Asn Gln Arg Tyr Gly Trp His Pro Ala Thr	
610 615 620	
gtg tgt aaa att cca cca ggc tgt aat ctg aag atc ttc aac aac cag	1920
Val Cys Lys Ile Pro Pro Gly Cys Asn Leu Lys Ile Phe Asn Asn Gln	
625 630 635 640	
gaa ttt gct gct ctt ctg gct cag tct gtt aat cag ggt ttt gaa gcc	1968
Glu Phe Ala Ala Leu Leu Ala Gln Ser Val Asn Gln Gly Phe Glu Ala	
645 650 655	
gtc tat cag cta act aga atg tgc acc ata aga atg agt ttt gtg aaa	2016
Val Tyr Gln Leu Thr Arg Met Cys Thr Ile Arg Met Ser Phe Val Lys	
660 665 670	

ggg tgg gga gca gaa tac cga agg cag acg gta aca agt act cct tgc 2064
 Gly Trp Gly Ala Glu Tyr Arg Arg Gln Thr Val Thr Ser Thr Pro Cys
 675 680 685
 tgg att gaa ctt cat ctg aat gga cct cta cag tgg ttg gac aaa gta 2112
 Trp Ile Glu Leu His Leu Asn Gly Pro Leu Gln Trp Leu Asp Lys Val
 690 695 700
 tta act cag atg gga tcc cct tca gtg cgt tgc tca agc atg tca taa 2160
 Leu Thr Gln Met Gly Ser Pro Ser Val Arg Cys Ser Ser Met Ser
 705 710 715

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 <213> Aequorea victoria and human

<400> 8

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 1 5 10 15
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
225 230 235 240

Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Thr Met Ser Ser Ile
245 250 255

Leu Pro Phe Thr Pro Pro Val Val Lys Arg Leu Leu Gly Trp Lys Lys
260 265 270

Ser Ala Gly Gly Ser Gly Gly Ala Gly Gly Gly Glu Gln Asn Gly Gln
275 280 285

Glu Glu Lys Trp Cys Glu Lys Ala Val Lys Ser Leu Val Lys Lys Leu
290 295 300

Lys Lys Thr Gly Arg Leu Asp Glu Leu Glu Lys Ala Ile Thr Thr Gln
305 310 315 320

Asn Cys Asn Thr Lys Cys Val Thr Ile Pro Ser Thr Cys Ser Glu Ile
325 330 335

Trp Gly Leu Ser Thr Pro Asn Thr Ile Asp Gln Trp Asp Thr Thr Gly
340 345 350

Leu Tyr Ser Phe Ser Glu Gln Thr Arg Ser Leu Asp Gly Arg Leu Gln
355 360 365

Val Ser His Arg Lys Gly Leu Pro His Val Ile Tyr Cys Arg Leu Trp
370 375 380

Arg Trp Pro Asp Leu His Ser His His Glu Leu Lys Ala Ile Glu Asn
385 390 395 400

Cys Glu Tyr Ala Phe Asn Leu Lys Lys Asp Glu Val Cys Val Asn Pro
405 410 415

Tyr His Tyr Gln Arg Val Glu Thr Pro Val Leu Pro Pro Val Leu Val
420 425 430

Pro Arg His Thr Glu Ile Leu Thr Glu Leu Pro Pro Leu Asp Asp Tyr
435 440 445

Thr His Ser Ile Pro Glu Asn Thr Asn Phe Pro Ala Gly Ile Glu Pro
450 455 460

Gln Ser Asn Tyr Ile Pro Glu Thr Pro Pro Pro Gly Tyr Ile Ser Glu
465 470 475 480

Asp Gly Glu Thr Ser Asp Gln Gln Leu Asn Gln Ser Met Asp Thr Gly
485 490 495

Ser Pro Ala Glu Leu Ser Pro Thr Thr Leu Ser Pro Val Asn His Ser
500 505 510

Leu Asp Leu Gln Pro Val Thr Tyr Ser Glu Pro Ala Phe Trp Cys Ser
515 520 525

Ile Ala Tyr Tyr Glu Leu Asn Gln Arg Val Gly Glu Thr Phe His Ala
530 535 540

Ser Gln Pro Ser Leu Thr Val Asp Gly Phe Thr Asp Pro Ser Asn Ser
545 550 555 560

Glu Arg Phe Cys Leu Gly Leu Leu Ser Asn Val Asn Arg Asn Ala Thr
565 570 575

Val Glu Met Thr Arg Arg His Ile Gly Arg Gly Val Arg Leu Tyr Tyr
580 585 590

Ile Gly Gly Glu Val Phe Ala Glu Cys Leu Ser Asp Ser Ala Ile Phe
595 600 605

Val Gln Ser Pro Asn Cys Asn Gln Arg Tyr Gly Trp His Pro Ala Thr
610 615 620

Val Cys Lys Ile Pro Pro Gly Cys Asn Leu Lys Ile Phe Asn Asn Gln
625 630 635 640

Glu Phe Ala Ala Leu Leu Ala Gln Ser Val Asn Gln Gly Phe Glu Ala
645 650 655

Val Tyr Gln Leu Thr Arg Met Cys Thr Ile Arg Met Ser Phe Val Lys
660 665 670

Gly Trp Gly Ala Glu Tyr Arg Arg Gln Thr Val Thr Ser Thr Pro Cys
675 680 685

Trp Ile Glu Leu His Leu Asn Gly Pro Leu Gln Trp Leu Asp Lys Val
690 695 700

Leu Thr Gln Met Gly Ser Pro Ser Val Arg Cys Ser Ser Met Ser
705 710 715

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<212> DNA
<213> Aequorea victoria and human

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Met Ser Ser Ile Leu Pro Phe Thr Pro Pro Val Val Lys Arg Leu Leu
1 5 10 15

gga tgg aag aag tca gct ggt ggg tct gga gga gca ggc gga gga gag 96
Gly Trp Lys Lys Ser Ala Gly Gly Ser Gly Gly Ala Gly Gly Gly Glu
20 25 30

cag aat ggg cag gaa gaa aag tgg tgt gag aaa gca gtg aaa agt ctg 144
Gln Asn Gly Gln Glu Glu Lys Trp Cys Glu Lys Ala Val Lys Ser Leu
35 40 45

gtg aag aag cta aag aaa aca gga cga tta gat gag ctt gag aaa gcc	192
Val Lys Lys Leu Lys Lys Thr Gly Arg Leu Asp Glu Leu Glu Lys Ala	
50 55 60	
atc acc act caa aac tgt aat act aaa tgt gtt acc ata cca agc act	240
Ile Thr Thr Gln Asn Cys Asn Thr Lys Cys Val Thr Ile Pro Ser Thr	
65 70 75 80	
tgc tct gaa att tgg gga ctg agt aca cca aat acg ata gat cag tgg	288
Cys Ser Glu Ile Trp Gly Leu Ser Thr Pro Asn Thr Ile Asp Gln Trp	
85 90 95	
gat aca aca ggc ctt tac agc ttc tct gaa caa acc agg tct ctt gat	336
Asp Thr Thr Gly Leu Tyr Ser Phe Ser Glu Gln Thr Arg Ser Leu Asp	
100 105 110	
ggt cgt ctc cag gta tcc cat cga aaa gga ttg cca cat gtt ata tat	384
Gly Arg Leu Gln Val Ser His Arg Lys Gly Leu Pro His Val Ile Tyr	
115 120 125	
tgc cga tta tgg cgc tgg cct gat ctt cac agt cat cat gaa ctc aag	432
Cys Arg Leu Trp Arg Trp Pro Asp Leu His Ser His His Glu Leu Lys	
130 135 140	
gca att gaa aac tgc gaa tat gct ttt aat ctt aaa aag gat gaa gta	480
Ala Ile Glu Asn Cys Glu Tyr Ala Phe Asn Leu Lys Lys Asp Glu Val	
145 150 155 160	
tgt gta aac cct tac cac tat cag aga gtt gag aca cca gtt ttg cct	528
Cys Val Asn Pro Tyr His Tyr Gln Arg Val Glu Thr Pro Val Leu Pro	
165 170 175	
cca gta tta gtg ccc cga cac acc gag atc cta aca gaa ctt ccg cct	576
Pro Val Leu Val Pro Arg His Thr Glu Ile Leu Thr Glu Leu Pro Pro	
180 185 190	
ctg gat gac tat act cac tcc att cca gaa aac act aac ttc cca gca	624
Leu Asp Asp Tyr Thr His Ser Ile Pro Glu Asn Thr Asn Phe Pro Ala	
195 200 205	
gga att gag cca cag agt aat tat att cca gaa acg cca cct cct gga	672
Gly Ile Glu Pro Gln Ser Asn Tyr Ile Pro Glu Thr Pro Pro Pro Gly	
210 215 220	
tat atc agt gaa gat gga gaa aca agt gac caa cag ttg aat caa agt	720
Tyr Ile Ser Glu Asp Gly Glu Thr Ser Asp Gln Gln Leu Asn Gln Ser	
225 230 235 240	
atg gac aca ggc tct cca gca gaa cta tct cct act act ctt tcc cct	768
Met Asp Thr Gly Ser Pro Ala Glu Leu Ser Pro Thr Thr Leu Ser Pro	
245 250 255	
gtt aat cat agc ttg gat tta cag cca gtt act tac tca gaa cct gca	816
Val Asn His Ser Leu Asp Leu Gln Pro Val Thr Tyr Ser Glu Pro Ala	
260 265 270	

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	1536
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
500 505 510	
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	1584
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
515 520 525	
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg	1632
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
530 535 540	
acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag cag	1680
Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln	
545 550 555 560	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	1728
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
565 570 575	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	1776
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
580 585 590	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	1824
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
595 600 605	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	1872
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
610 615 620	
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	1920
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
625 630 635 640	
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg	1968
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val	
645 650 655	
cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc	2016
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro	
660 665 670	
gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc	2064
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser	
675 680 685	
aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg	2112
Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val	
690 695 700	
acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag taa	2157
Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
705 710 715	

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 <212> PRT
 <213> Aequorea victoria and human

<400> 10

Met Ser Ser Ile Leu Pro Phe Thr Pro Pro Val Val Lys Arg Leu Leu
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Gly Trp Lys Lys Ser Ala Gly Gly Ser Gly Gly Ala Gly Gly Gly Glu
 20 25 30

Gln Asn Gly Gln Glu Glu Lys Trp Cys Glu Lys Ala Val Lys Ser Leu
 35 40 45

Val Lys Lys Leu Lys Lys Thr Gly Arg Leu Asp Glu Leu Glu Lys Ala
 50 55 60

Ile Thr Thr Gln Asn Cys Asn Thr Lys Cys Val Thr Ile Pro Ser Thr
 65 70 75 80

Cys Ser Glu Ile Trp Gly Leu Ser Thr Pro Asn Thr Ile Asp Gln Trp
 85 90 95

Asp Thr Thr Gly Leu Tyr Ser Phe Ser Glu Gln Thr Arg Ser Leu Asp
 100 105 110

Gly Arg Leu Gln Val Ser His Arg Lys Gly Leu Pro His Val Ile Tyr
 115 120 125

Cys Arg Leu Trp Arg Trp Pro Asp Leu His Ser His His Glu Leu Lys
 130 135 140

Ala Ile Glu Asn Cys Glu Tyr Ala Phe Asn Leu Lys Lys Asp Glu Val
 145 150 155 160

Cys Val Asn Pro Tyr His Tyr Gln Arg Val Glu Thr Pro Val Leu Pro
 165 170 175

Pro Val Leu Val Pro Arg His Thr Glu Ile Leu Thr Glu Leu Pro Pro
 180 185 190

Leu Asp Asp Tyr Thr His Ser Ile Pro Glu Asn Thr Asn Phe Pro Ala
195 200 205

Gly Ile Glu Pro Gln Ser Asn Tyr Ile Pro Glu Thr Pro Pro Pro Gly
210 215 220

Tyr Ile Ser Glu Asp Gly Glu Thr Ser Asp Gln Gln Leu Asn Gln Ser
225 230 235 240

Met Asp Thr Gly Ser Pro Ala Glu Leu Ser Pro Thr Thr Leu Ser Pro
245 250 255

Val Asn His Ser Leu Asp Leu Gln Pro Val Thr Tyr Ser Glu Pro Ala
260 265 270

Phe Trp Cys Ser Ile Ala Tyr Tyr Glu Leu Asn Gln Arg Val Gly Glu
275 280 285

Thr Phe His Ala Ser Gln Pro Ser Leu Thr Val Asp Gly Phe Thr Asp
290 295 300

Pro Ser Asn Ser Glu Arg Phe Cys Leu Gly Leu Leu Ser Asn Val Asn
305 310 315 320

Arg Asn Ala Thr Val Glu Met Thr Arg Arg His Ile Gly Arg Gly Val
325 330 335

Arg Leu Tyr Tyr Ile Gly Gly Glu Val Phe Ala Glu Cys Leu Ser Asp
340 345 350

Ser Ala Ile Phe Val Gln Ser Pro Asn Cys Asn Gln Arg Tyr Gly Trp
355 360 365

His Pro Ala Thr Val Cys Lys Ile Pro Pro Gly Cys Asn Leu Lys Ile
370 375 380

Phe Asn Asn Gln Glu Phe Ala Ala Leu Leu Ala Gln Ser Val Asn Gln
385 390 395 400

Gly Phe Glu Ala Val Tyr Gln Leu Thr Arg Met Cys Thr Ile Arg Met
405 410 415

Ser Phe Val Lys Gly Trp Gly Ala Glu Tyr Arg Arg Gln Thr Val Thr
 420 425 430

Ser Thr Pro Cys Trp Ile Glu Leu His Leu Asn Gly Pro Leu Gln Trp
 435 440 445

Leu Asp Lys Val Leu Thr Gln Met Gly Ser Pro Ser Val Arg Cys Ser
 450 455 460

Ser Met Ser Trp Val Pro Arg Ala Arg Asp Pro Pro Val Ala Thr Met
 465 470 475 480

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 485 490 495

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 500 505 510

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 515 520 525

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 530 535 540

Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
 545 550 555 560

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 565 570 575

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 580 585 590

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 595 600 605

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 610 615 620

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 625 630 635 640

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
645 650 655

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
660 665 670

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
675 680 685

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
690 695 700

Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
705 710 715

<210> 11
<211> 1908
<212> DNA
<213> Aequorea victoria and human

<220>
<221> CDS
<222> (1)..(1908)
<223>

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gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60
ctg acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag 240
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80
cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
130 135 140	
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac	480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
145 150 155 160	
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc	528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
165 170 175	
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc	576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	
180 185 190	
ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg	624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	
195 200 205	
agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc	672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	
210 215 220	
gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag tcc	720
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser	
225 230 235 240	
gga ctc aga tct cga gct caa gct tcc atg agc gag acg gtc atc atg	768
Gly Leu Arg Ser Arg Ala Gln Ala Ser Met Ser Glu Thr Val Ile Met	
245 250 255	
agc gag acg gtc atc tgt tcc agc cgg gcc act gtg atg ctt tat gat	816
Ser Glu Thr Val Ile Cys Ser Ser Arg Ala Thr Val Met Leu Tyr Asp	
260 265 270	
gat ggc aac aag cga tgg ctc cct gct ggc acg ggt ccc cag gcc ttc	864
Asp Gly Asn Lys Arg Trp Leu Pro Ala Gly Thr Gly Pro Gln Ala Phe	
275 280 285	
agc cgc gtc cag atc tac cac aac ccc acg gcc aat tcc ttt cgc gtc	912
Ser Arg Val Gln Ile Tyr His Asn Pro Thr Ala Asn Ser Phe Arg Val	
290 295 300	
gtg ggc cgg aag atg cag ccc gac cag cag gtg gtc atc aac tgt gcc	960
Val Gly Arg Lys Met Gln Pro Asp Gln Gln Val Val Ile Asn Cys Ala	
305 310 315 320	

atc gtc cgg ggt gtc aag tat aac cag gcc acc ccc aac ttc cat cag Ile Val Arg Gly Val Lys Tyr Asn Gln Ala Thr Pro Asn Phe His Gln 325 330 335	1008
tgg cgc gac gct cgc cag gtc tgg ggc ctc aac ttc ggc agc aag gag Trp Arg Asp Ala Arg Gln Val Trp Gly Leu Asn Phe Gly Ser Lys Glu 340 345 350	1056
gat gcg gcc cag ttt gcc gcc ggc atg gcc agt gcc cta gag gcg ttg Asp Ala Ala Gln Phe Ala Ala Gly Met Ala Ser Ala Leu Glu Ala Leu 355 360 365	1104
gaa gga ggt ggg ccc cct cca ccc cca gca ctt ccc acc tgg tcg gtc Glu Gly Gly Gly Pro Pro Pro Pro Pro Ala Leu Pro Thr Trp Ser Val 370 375 380	1152
ccg aac ggc ccc tcc ccg gag gag gtg gag cag cag aaa agg cag cag Pro Asn Gly Pro Ser Pro Glu Glu Val Glu Gln Gln Lys Arg Gln Gln 385 390 395 400	1200
ccc ggc ccg tcg gag cac ata gag cgc ccg gtc tcc aat gca gga ggc Pro Gly Pro Ser Glu His Ile Glu Arg Arg Val Ser Asn Ala Gly Gly 405 410 415	1248
cca cct gct ccc ccc gct ggg ggt cca ccc cca cca cca gga cct ccc Pro Pro Ala Pro Pro Ala Gly Gly Pro Pro Pro Pro Pro Gly Pro Pro 420 425 430	1296
cct cct cca ggt ccc ccc cca ccc cca ggt ttg ccc cct tcg ggg gtc Pro Pro Pro Gly Pro Pro Pro Pro Pro Gly Leu Pro Pro Ser Gly Val 435 440 445	1344
cca gct gca gcg cac gga gca ggg gga gga cca ccc cct gca ccc cct Pro Ala Ala Ala His Gly Ala Gly Gly Gly Pro Pro Pro Ala Pro Pro 450 455 460	1392
ctc ccg gca gca cag ggc cct ggt ggt ggg gga gct ggg gcc cca ggc Leu Pro Ala Ala Gln Gly Pro Gly Gly Gly Ala Gly Ala Pro Gly 465 470 475 480	1440
ctg gcc gca gct att gct gga gcc aaa ctc agg aaa gtc agc aag cag Leu Ala Ala Ala Ile Ala Gly Ala Lys Leu Arg Lys Val Ser Lys Gln 485 490 495	1488
gag gag gcc tca ggg ggg ccc aca gcc ccc aaa gct gag agt ggt cga Glu Glu Ala Ser Gly Gly Pro Thr Ala Pro Lys Ala Glu Ser Gly Arg 500 505 510	1536
agc gga ggt ggg gga ctc atg gaa gag atg aac gcc atg ctg gcc cgg Ser Gly Gly Gly Gly Leu Met Glu Glu Met Asn Ala Met Leu Ala Arg 515 520 525	1584
aga agg aaa gcc acg caa gtt ggg gag aaa acc ccc aag gat gaa tct Arg Arg Lys Ala Thr Gln Val Gly Glu Lys Thr Pro Lys Asp Glu Ser 530 535 540	1632

gcc aat cag gag gag cca gag gcc aga gtc ccg gcc cag agt gaa tct 1680
 Ala Asn Gln Glu Glu Pro Glu Ala Arg Val Pro Ala Gln Ser Glu Ser
 545 550 555 560

gtg cgg aga ccc tgg gag aag aac agc aca acc ttg cca agg atg aag 1728
 Val Arg Arg Pro Trp Glu Lys Asn Ser Thr Thr Leu Pro Arg Met Lys
 565 570 575

tcg tct tct tcg gtg acc act tcc gag acc caa ccc tgc acg ccc agc 1776
 Ser Ser Ser Ser Val Thr Thr Ser Glu Thr Gln Pro Cys Thr Pro Ser
 580 585 590

tcc agt gat tac tcg gac cta cag agg gtg aaa cag gag ctt ctg gaa 1824
 Ser Ser Asp Tyr Ser Asp Leu Gln Arg Val Lys Gln Glu Leu Leu Glu
 595 600 605

gag gtg aag aag gaa ttg cag aaa gtg aaa gag gaa atc att gaa gcc 1872
 Glu Val Lys Lys Glu Leu Gln Lys Val Lys Glu Glu Ile Ile Glu Ala
 610 615 620

ttc gtc cag gag ctg agg aag cgg ggt tct ccc tga 1908
 Phe Val Gln Glu Leu Arg Lys Arg Gly Ser Pro
 625 630 635

<210> 12
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 <213> Aequorea victoria and human

<400> 12

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
225 230 235 240

Gly Leu Arg Ser Arg Ala Gln Ala Ser Met Ser Glu Thr Val Ile Met
245 250 255

Ser Glu Thr Val Ile Cys Ser Ser Arg Ala Thr Val Met Leu Tyr Asp
260 265 270

Asp Gly Asn Lys Arg Trp Leu Pro Ala Gly Thr Gly Pro Gln Ala Phe
275 280 285

Ser Arg Val Gln Ile Tyr His Asn Pro Thr Ala Asn Ser Phe Arg Val
290 295 300

Val Gly Arg Lys Met Gln Pro Asp Gln Gln Val Val Ile Asn Cys Ala
305 310 315 320

Ile Val Arg Gly Val Lys Tyr Asn Gln Ala Thr Pro Asn Phe His Gln
325 330 335

Trp Arg Asp Ala Arg Gln Val Trp Gly Leu Asn Phe Gly Ser Lys Glu
340 345 350

Asp Ala Ala Gln Phe Ala Ala Gly Met Ala Ser Ala Leu Glu Ala Leu
355 360 365

Glu Gly Gly Gly Pro Pro Pro Pro Pro Ala Leu Pro Thr Trp Ser Val
370 375 380

Pro Asn Gly Pro Ser Pro Glu Glu Val Glu Gln Gln Lys Arg Gln Gln
385 390 395 400

Pro Gly Pro Ser Glu His Ile Glu Arg Arg Val Ser Asn Ala Gly Gly
405 410 415

Pro Pro Ala Pro Pro Ala Gly Gly Pro Pro Pro Pro Pro Gly Pro Pro
420 425 430

Pro Pro Pro Gly Pro Pro Pro Pro Pro Gly Leu Pro Pro Ser Gly Val
435 440 445

Pro Ala Ala Ala His Gly Ala Gly Gly Gly Pro Pro Pro Ala Pro Pro
450 455 460

Leu Pro Ala Ala Gln Gly Pro Gly Gly Gly Gly Ala Gly Ala Pro Gly
465 470 475 480

Leu Ala Ala Ala Ile Ala Gly Ala Lys Leu Arg Lys Val Ser Lys Gln
485 490 495

Glu Glu Ala Ser Gly Gly Pro Thr Ala Pro Lys Ala Glu Ser Gly Arg
500 505 510

Ser Gly Gly Gly Gly Leu Met Glu Glu Met Asn Ala Met Leu Ala Arg
515 520 525

Arg Arg Lys Ala Thr Gln Val Gly Glu Lys Thr Pro Lys Asp Glu Ser
530 535 540

Ala Asn Gln Glu Glu Pro Glu Ala Arg Val Pro Ala Gln Ser Glu Ser
545 550 555 560

Val Arg Arg Pro Trp Glu Lys Asn Ser Thr Thr Leu Pro Arg Met Lys
565 570 575

Ser Ser Ser Ser Val Thr Thr Ser Glu Thr Gln Pro Cys Thr Pro Ser
580 585 590

Ser Ser Asp Tyr Ser Asp Leu Gln Arg Val Lys Gln Glu Leu Leu Glu
595 600 605

Glu Val Lys Lys Glu Leu Gln Lys Val Lys Glu Glu Ile Ile Glu Ala
610 615 620

Phe Val Gln Glu Leu Arg Lys Arg Gly Ser Pro
625 630 635

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gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ctg acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag 240
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

ccc acc atc aag atc aat ggc tac aca gga cca ggg aca gtg cgc atc	960
Pro Thr Ile Lys Ile Asn Gly Tyr Thr Gly Pro Gly Thr Val Arg Ile	
305 310 315 320	
tcc ctg gtc acc aag gac cct cct cac cgg cct cac ccc cac gag ctt	1008
Ser Leu Val Thr Lys Asp Pro Pro His Arg Pro His Pro His Glu Leu	
325 330 335	
gta gga aag gac tgc cgg gat ggc ttc tat gag gct gag ctc tgc ccg	1056
Val Gly Lys Asp Cys Arg Asp Gly Phe Tyr Glu Ala Glu Leu Cys Pro	
340 345 350	
gac cgc tgc atc cac agt ttc cag aac ctg gga atc cag tgt gtg aag	1104
Asp Arg Cys Ile His Ser Phe Gln Asn Leu Gly Ile Gln Cys Val Lys	
355 360 365	
aag cgg gac ctg gag cag gct atc agt cag cgc atc cag acc aac aac	1152
Lys Arg Asp Leu Glu Gln Ala Ile Ser Gln Arg Ile Gln Thr Asn Asn	
370 375 380	
aac ccc ttc caa gtt cct ata gaa gag cag cgt ggg gac tac gac ctg	1200
Asn Pro Phe Gln Val Pro Ile Glu Glu Gln Arg Gly Asp Tyr Asp Leu	
385 390 395 400	
aat gct gtg cgg ctc tgc ttc cag gtg aca gtg cgg gac cca tca ggc	1248
Asn Ala Val Arg Leu Cys Phe Gln Val Thr Val Arg Asp Pro Ser Gly	
405 410 415	
agg ccc ctc cgc ctg ccg cct gtc ctt cct cat ccc atc ttt gac aat	1296
Arg Pro Leu Arg Leu Pro Pro Val Leu Pro His Pro Ile Phe Asp Asn	
420 425 430	
cgt gcc ccc aac act gcc gag ctc aag atc tgc cga gtg aac cga aac	1344
Arg Ala Pro Asn Thr Ala Glu Leu Lys Ile Cys Arg Val Asn Arg Asn	
435 440 445	
tct ggc agc tgc ctc ggt ggg gat gag atc ttc cta ctg tgt gac aag	1392
Ser Gly Ser Cys Leu Gly Gly Asp Glu Ile Phe Leu Leu Cys Asp Lys	
450 455 460	
gtg cag aaa gag gac att gag gtg tat ttc acg gga cca ggc tgg gag	1440
Val Gln Lys Glu Asp Ile Glu Val Tyr Phe Thr Gly Pro Gly Trp Glu	
465 470 475 480	
gcc cga ggc tcc ttt tcg caa gct gat gtg cac cga caa gtg gcc att	1488
Ala Arg Gly Ser Phe Ser Gln Ala Asp Val His Arg Gln Val Ala Ile	
485 490 495	
gtg ttc cgg acc cct ccc tac gca gac ccc agc ctg cag gct cct gtg	1536
Val Phe Arg Thr Pro Pro Tyr Ala Asp Pro Ser Leu Gln Ala Pro Val	
500 505 510	
cgt gtc tcc atg cag ctg cgg cgg cct tcc gac cgg gag ctc agt gag	1584
Arg Val Ser Met Gln Leu Arg Arg Pro Ser Asp Arg Glu Leu Ser Glu	
515 520 525	

ccc atg gaa ttc cag tac ctg cca gat aca gac gat cgt cac cgg att	1632
Pro Met Glu Phe Gln Tyr Leu Pro Asp Thr Asp Asp Arg His Arg Ile	
530 535 540	
gag gag aaa cgt aaa agg aca tat gag acc ttc aag agc atc atg aag	1680
Glu Glu Lys Arg Lys Arg Thr Tyr Glu Thr Phe Lys Ser Ile Met Lys	
545 550 555 560	
aag agt cct ttc agc gga ccc acc gac ccc cgg cct cca cct cga cgc	1728
Lys Ser Pro Phe Ser Gly Pro Thr Asp Pro Arg Pro Pro Pro Arg Arg	
565 570 575	
att gct gtg cct tcc cgc agc tca gct tct gtc ccc aag cca gca ccc	1776
Ile Ala Val Pro Ser Arg Ser Ser Ala Ser Val Pro Lys Pro Ala Pro	
580 585 590	
cag ccc tat ccc ttt acg tca tcc ctg agc acc atc aac tat gat gag	1824
Gln Pro Tyr Pro Phe Thr Ser Ser Leu Ser Thr Ile Asn Tyr Asp Glu	
595 600 605	
ttt ccc acc atg gtg ttt cct tct ggg cag atc agc cag gcc tcg gcc	1872
Phe Pro Thr Met Val Phe Pro Ser Gly Gln Ile Ser Gln Ala Ser Ala	
610 615 620	
ttg gcc ccg gcc cct ccc caa gtc ctg ccc cag gct cca gcc cct gcc	1920
Leu Ala Pro Ala Pro Pro Gln Val Leu Pro Gln Ala Pro Ala Pro Ala	
625 630 635 640	
cct gct cca gcc atg gta tca gct ctg gcc cag gcc cca gcc cct gtc	1968
Pro Ala Pro Ala Met Val Ser Ala Leu Ala Gln Ala Pro Ala Pro Val	
645 650 655	
cca gtc cta gcc cca ggc cct cct cag gct gtg gcc cca cct gcc ccc	2016
Pro Val Leu Ala Pro Gly Pro Pro Gln Ala Val Ala Pro Ala Pro	
660 665 670	
aag ccc acc cag gct ggg gaa gga acg ctg tca gag gcc ctg ctg cag	2064
Lys Pro Thr Gln Ala Gly Glu Gly Thr Leu Ser Glu Ala Leu Leu Gln	
675 680 685	
ctg cag ttt gat gat gaa gac ctg ggg gcc ttg ctt ggc aac agc aca	2112
Leu Gln Phe Asp Asp Glu Asp Leu Gly Ala Leu Leu Gly Asn Ser Thr	
690 695 700	
gac cca gct gtg ttc aca gac ctg gca tcc gtc gac aac tcc gag ttt	2160
Asp Pro Ala Val Phe Thr Asp Leu Ala Ser Val Asp Asn Ser Glu Phe	
705 710 715 720	
cag cag ctg ctg aac cag ggc ata cct gtg gcc ccc cac aca act gag	2208
Gln Gln Leu Leu Asn Gln Gly Ile Pro Val Ala Pro His Thr Thr Glu	
725 730 735	
ccc atg ctg atg gag tac cct gag gct ata act cgc cta gtg aca ggg	2256
Pro Met Leu Met Glu Tyr Pro Glu Ala Ile Thr Arg Leu Val Thr Gly	
740 745 750	

gcc cag agg ccc ccc gac cca gct cct gct cca ctg ggg gcc ccg ggg 2304
 Ala Gln Arg Pro Pro Asp Pro Ala Pro Ala Pro Leu Gly Ala Pro Gly
 755 760 765

ctc ccc aat ggc ctc ctt tca gga gat gaa gac ttc tcc tcc att gcg 2352
 Leu Pro Asn Gly Leu Leu Ser Gly Asp Glu Asp Phe Ser Ser Ile Ala
 770 775 780

gac atg gac ttc tca gcc ctg ctg agt cag atc agc tcc taa 2394
 Asp Met Asp Phe Ser Ala Leu Leu Ser Gln Ile Ser Ser
 785 790 795

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 <211> 797
 <212> PRT
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<400> 14

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 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
225 230 235 240

Gly Leu Arg Ser Arg Ala Met Asp Glu Leu Phe Pro Leu Ile Phe Pro
245 250 255

Ala Glu Pro Ala Gln Ala Ser Gly Pro Tyr Val Glu Ile Ile Glu Gln
260 265 270

Pro Lys Gln Arg Gly Met Arg Phe Arg Tyr Lys Cys Glu Gly Arg Ser
275 280 285

Ala Gly Ser Ile Pro Gly Glu Arg Ser Thr Asp Thr Thr Lys Thr His
290 295 300

Pro Thr Ile Lys Ile Asn Gly Tyr Thr Gly Pro Gly Thr Val Arg Ile
305 310 315 320

Ser Leu Val Thr Lys Asp Pro Pro His Arg Pro His Pro His Glu Leu
325 330 335

Val Gly Lys Asp Cys Arg Asp Gly Phe Tyr Glu Ala Glu Leu Cys Pro
340 345 350

Asp Arg Cys Ile His Ser Phe Gln Asn Leu Gly Ile Gln Cys Val Lys
355 360 365

Lys Arg Asp Leu Glu Gln Ala Ile Ser Gln Arg Ile Gln Thr Asn Asn
370 375 380

Asn Pro Phe Gln Val Pro Ile Glu Glu Gln Arg Gly Asp Tyr Asp Leu
385 390 395 400

Asn Ala Val Arg Leu Cys Phe Gln Val Thr Val Arg Asp Pro Ser Gly
405 410 415

Arg Pro Leu Arg Leu Pro Pro Val Leu Pro His Pro Ile Phe Asp Asn
420 425 430

Arg Ala Pro Asn Thr Ala Glu Leu Lys Ile Cys Arg Val Asn Arg Asn
435 440 445

Ser Gly Ser Cys Leu Gly Gly Asp Glu Ile Phe Leu Leu Cys Asp Lys
450 455 460

Val Gln Lys Glu Asp Ile Glu Val Tyr Phe Thr Gly Pro Gly Trp Glu
465 470 475 480

Ala Arg Gly Ser Phe Ser Gln Ala Asp Val His Arg Gln Val Ala Ile
485 490 495

Val Phe Arg Thr Pro Pro Tyr Ala Asp Pro Ser Leu Gln Ala Pro Val
500 505 510

Arg Val Ser Met Gln Leu Arg Arg Pro Ser Asp Arg Glu Leu Ser Glu
515 520 525

Pro Met Glu Phe Gln Tyr Leu Pro Asp Thr Asp Asp Arg His Arg Ile
530 535 540

Glu Glu Lys Arg Lys Arg Thr Tyr Glu Thr Phe Lys Ser Ile Met Lys
545 550 555 560

Lys Ser Pro Phe Ser Gly Pro Thr Asp Pro Arg Pro Pro Pro Arg Arg
565 570 575

Ile Ala Val Pro Ser Arg Ser Ser Ala Ser Val Pro Lys Pro Ala Pro
580 585 590

Gln Pro Tyr Pro Phe Thr Ser Ser Leu Ser Thr Ile Asn Tyr Asp Glu
595 600 605

Phe Pro Thr Met Val Phe Pro Ser Gly Gln Ile Ser Gln Ala Ser Ala
610 615 620

Leu Ala Pro Ala Pro Pro Gln Val Leu Pro Gln Ala Pro Ala Pro Ala
625 630 635 640

Pro Ala Pro Ala Met Val Ser Ala Leu Ala Gln Ala Pro Ala Pro Val
645 650 655

Pro Val Leu Ala Pro Gly Pro Pro Gln Ala Val Ala Pro Pro Ala Pro
660 665 670

Lys Pro Thr Gln Ala Gly Glu Gly Thr Leu Ser Glu Ala Leu Leu Gln
675 680 685

Leu Gln Phe Asp Asp Glu Asp Leu Gly Ala Leu Leu Gly Asn Ser Thr
690 695 700

Asp Pro Ala Val Phe Thr Asp Leu Ala Ser Val Asp Asn Ser Glu Phe
705 710 715 720

Gln Gln Leu Leu Asn Gln Gly Ile Pro Val Ala Pro His Thr Thr Glu
725 730 735

Pro Met Leu Met Glu Tyr Pro Glu Ala Ile Thr Arg Leu Val Thr Gly
740 745 750

Ala Gln Arg Pro Pro Asp Pro Ala Pro Ala Pro Leu Gly Ala Pro Gly
755 760 765

Leu Pro Asn Gly Leu Leu Ser Gly Asp Glu Asp Phe Ser Ser Ile Ala
770 775 780

Asp Met Asp Phe Ser Ala Leu Leu Ser Gln Ile Ser Ser
785 790 795

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<212> DNA
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 <222> (1)..(2394)
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 tct ggc ccc tat gtg gag atc att gag cag ccc aag cag cgg ggc atg 96
 Ser Gly Pro Tyr Val Glu Ile Ile Glu Gln Pro Lys Gln Arg Gly Met
 20 25 30
 cgc ttc cgc tac aag tgc gag ggg cgc tcc gcg ggc agc atc cca ggc 144
 Arg Phe Arg Tyr Lys Cys Glu Gly Arg Ser Ala Gly Ser Ile Pro Gly
 35 40 45
 gag agg agc aca gat acc acc aag acc cac ccc acc atc aag atc aat 192
 Glu Arg Ser Thr Asp Thr Thr Lys Thr His Pro Thr Ile Lys Ile Asn
 50 55 60
 ggc tac aca gga cca ggg aca gtg cgc atc tcc ctg gtc acc aag gac 240
 Gly Tyr Thr Gly Pro Gly Thr Val Arg Ile Ser Leu Val Thr Lys Asp
 65 70 75 80
 cct cct cac cgg cct cac ccc cac gag ctt gta gga aag gac tgc cgg 288
 Pro Pro His Arg Pro His Pro His Glu Leu Val Gly Lys Asp Cys Arg
 85 90 95
 gat ggc ttc tat gag gct gag ctc tgc ccg gac cgc tgc atc cac agt 336
 Asp Gly Phe Tyr Glu Ala Glu Leu Cys Pro Asp Arg Cys Ile His Ser
 100 105 110
 ttc cag aac ctg gga atc cag tgt gtg aag aag cgg gac ctg gag cag 384
 Phe Gln Asn Leu Gly Ile Gln Cys Val Lys Lys Arg Asp Leu Glu Gln
 115 120 125
 gct atc agt cag cgc atc cag acc aac aac aac ccc ttc caa gtt cct 432
 Ala Ile Ser Gln Arg Ile Gln Thr Asn Asn Asn Pro Phe Gln Val Pro
 130 135 140
 ata gaa gag cag cgt ggg gac tac gac ctg aat gct gtg cgg ctc tgc 480
 Ile Glu Glu Gln Arg Gly Asp Tyr Asp Leu Asn Ala Val Arg Leu Cys
 145 150 155 160
 ttc cag gtg aca gtg cgg gac cca tca ggc agg ccc ctc cgc ctg ccg 528
 Phe Gln Val Thr Val Arg Asp Pro Ser Gly Arg Pro Leu Arg Leu Pro
 165 170 175
 cct gtc ctt cct cat ccc atc ttt gac aat cgt gcc ccc aac act gcc 576
 Pro Val Leu Pro His Pro Ile Phe Asp Asn Arg Ala Pro Asn Thr Ala
 180 185 190

cct cct cag gct gtg gcc cca cct gcc ccc aag ccc acc cag gct ggg Pro Pro Gln Ala Val Ala Pro Pro Ala Pro Lys Pro Thr Gln Ala Gly 420 425 430	1296
gaa gga acg ctg tca gag gcc ctg ctg cag ctg cag ttt gat gat gaa Glu Gly Thr Leu Ser Glu Ala Leu Leu Gln Leu Gln Phe Asp Asp Glu 435 440 445	1344
gac ctg ggg gcc ttg ctt ggc aac agc aca gac cca gct gtg ttc aca Asp Leu Gly Ala Leu Leu Gly Asn Ser Thr Asp Pro Ala Val Phe Thr 450 455 460	1392
gac ctg gca tcc gtc gac aac tcc gag ttt cag cag ctg ctg aac cag Asp Leu Ala Ser Val Asp Asn Ser Glu Phe Gln Gln Leu Leu Asn Gln 465 470 475 480	1440
ggc ata cct gtg gcc ccc cac aca act gag ccc atg ctg atg gag tac Gly Ile Pro Val Ala Pro His Thr Thr Glu Pro Met Leu Met Glu Tyr 485 490 495	1488
cct gag gct ata act cgc cta gtg aca ggg gcc cag agg ccc ccc gac Pro Glu Ala Ile Thr Arg Leu Val Thr Gly Ala Gln Arg Pro Pro Asp 500 505 510	1536
cca gct cct gct cca ctg ggg gcc ccg ggg ctc ccc aat ggc ctc ctt Pro Ala Pro Ala Pro Leu Gly Ala Pro Gly Leu Pro Asn Gly Leu Leu 515 520 525	1584
tca gga gat gaa gac ttc tcc tcc att gcg gac atg gac ttc tca gcc Ser Gly Asp Glu Asp Phe Ser Ser Ile Ala Asp Met Asp Phe Ser Ala 530 535 540	1632
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ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag ggc Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly 580 585 590	1776
gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc acc Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr 595 600 605	1824
acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg acc Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr 610 615 620	1872
tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag cag cac Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His 625 630 635 640	1920

Arg Phe Arg Tyr Lys Cys Glu Gly Arg Ser Ala Gly Ser Ile Pro Gly
35 40 45

Glu Arg Ser Thr Asp Thr Thr Lys Thr His Pro Thr Ile Lys Ile Asn
50 55 60

Gly Tyr Thr Gly Pro Gly Thr Val Arg Ile Ser Leu Val Thr Lys Asp
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Pro Pro His Arg Pro His Pro His Glu Leu Val Gly Lys Asp Cys Arg
85 90 95

Asp Gly Phe Tyr Glu Ala Glu Leu Cys Pro Asp Arg Cys Ile His Ser
100 105 110

Phe Gln Asn Leu Gly Ile Gln Cys Val Lys Lys Arg Asp Leu Glu Gln
115 120 125

Ala Ile Ser Gln Arg Ile Gln Thr Asn Asn Asn Pro Phe Gln Val Pro
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Ile Glu Glu Gln Arg Gly Asp Tyr Asp Leu Asn Ala Val Arg Leu Cys
145 150 155 160

Phe Gln Val Thr Val Arg Asp Pro Ser Gly Arg Pro Leu Arg Leu Pro
165 170 175

Pro Val Leu Pro His Pro Ile Phe Asp Asn Arg Ala Pro Asn Thr Ala
180 185 190

Glu Leu Lys Ile Cys Arg Val Asn Arg Asn Ser Gly Ser Cys Leu Gly
195 200 205

Gly Asp Glu Ile Phe Leu Leu Cys Asp Lys Val Gln Lys Glu Asp Ile
210 215 220

Glu Val Tyr Phe Thr Gly Pro Gly Trp Glu Ala Arg Gly Ser Phe Ser
225 230 235 240

Gln Ala Asp Val His Arg Gln Val Ala Ile Val Phe Arg Thr Pro Pro
245 250 255

Tyr Ala Asp Pro Ser Leu Gln Ala Pro Val Arg Val Ser Met Gln Leu
260 265 270

Arg Arg Pro Ser Asp Arg Glu Leu Ser Glu Pro Met Glu Phe Gln Tyr
275 280 285

Leu Pro Asp Thr Asp Asp Arg His Arg Ile Glu Glu Lys Arg Lys Arg
290 295 300

Thr Tyr Glu Thr Phe Lys Ser Ile Met Lys Lys Ser Pro Phe Ser Gly
305 310 315 320

Pro Thr Asp Pro Arg Pro Pro Pro Arg Arg Ile Ala Val Pro Ser Arg
325 330 335

Ser Ser Ala Ser Val Pro Lys Pro Ala Pro Gln Pro Tyr Pro Phe Thr
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Ser Ser Leu Ser Thr Ile Asn Tyr Asp Glu Phe Pro Thr Met Val Phe
355 360 365

Pro Ser Gly Gln Ile Ser Gln Ala Ser Ala Leu Ala Pro Ala Pro Pro
370 375 380

Gln Val Leu Pro Gln Ala Pro Ala Pro Ala Pro Ala Pro Ala Met Val
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Pro Pro Gln Ala Val Ala Pro Pro Ala Pro Lys Pro Thr Gln Ala Gly
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Glu Gly Thr Leu Ser Glu Ala Leu Leu Gln Leu Gln Phe Asp Asp Glu
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Asp Leu Ala Ser Val Asp Asn Ser Glu Phe Gln Gln Leu Leu Asn Gln
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Gly Ile Pro Val Ala Pro His Thr Thr Glu Pro Met Leu Met Glu Tyr
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Pro Glu Ala Ile Thr Arg Leu Val Thr Gly Ala Gln Arg Pro Pro Asp
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Pro Ala Pro Ala Pro Leu Gly Ala Pro Gly Leu Pro Asn Gly Leu Leu
 515 520 525

Ser Gly Asp Glu Asp Phe Ser Ser Ile Ala Asp Met Asp Phe Ser Ala
 530 535 540

Leu Leu Ser Gln Ile Ser Ser Leu Asp Pro Pro Val Ala Thr Met Val
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Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu
 565 570 575

Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly
 580 585 590

Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr
 595 600 605

Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr
 610 615 620

Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His
 625 630 635 640

Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr
 645 650 655

Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys
 660 665 670

Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp
 675 680 685

Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr
 690 695 700

Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile
705 710 715 720

Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln
725 730 735

Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val
740 745 750

Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys
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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
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gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ctg acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag 240
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
130 135 140	
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac	480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
145 150 155 160	
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc	528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
165 170 175	
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc	576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	
180 185 190	
ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg	624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	
195 200 205	
agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc	672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	
210 215 220	
gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag tcc	720
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser	
225 230 235 240	
gga ctc aga tct cga ggc aag atg gct gac ccg gct gcg ggg ccg ccg	768
Gly Leu Arg Ser Arg Gly Lys Met Ala Asp Pro Ala Ala Gly Pro Pro	
245 250 255	
ccg agc gag ggc gag gag agc acc gtg cgc ttc gcc cgc aaa ggc gcc	816
Pro Ser Glu Gly Glu Glu Ser Thr Val Arg Phe Ala Arg Lys Gly Ala	
260 265 270	
ctc cgg cag aag aac gtg cat gag gtc aag aac cac aaa ttc acc gcc	864
Leu Arg Gln Lys Asn Val His Glu Val Lys Asn His Lys Phe Thr Ala	
275 280 285	
cgc ttc ttc aag cag ccc acc ttc tgc agc cac tgc acc gac ttc atc	912
Arg Phe Phe Lys Gln Pro Thr Phe Cys Ser His Cys Thr Asp Phe Ile	
290 295 300	

gaa ggc gag tac ttc aat gtg cct gtg cca cca gaa gga agt gag gcc Glu Gly Glu Tyr Phe Asn Val Pro Val Pro Pro Glu Gly Ser Glu Ala 530 535 540	1632
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ctc gat tct gag gga cac atc aag att gcc gat ttt ggc atg tgt aag Leu Asp Ser Glu Gly His Ile Lys Ile Ala Asp Phe Gly Met Cys Lys 725 730 735	2208
gaa aac atc tgg gat ggg gtg aca acc aag aca ttc tgt ggc act cca Glu Asn Ile Trp Asp Gly Val Thr Thr Lys Thr Phe Cys Gly Thr Pro 740 745 750	2256

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
225 230 235 240

Gly Leu Arg Ser Arg Gly Lys Met Ala Asp Pro Ala Ala Gly Pro Pro
 245 250 255

Pro Ser Glu Gly Glu Glu Ser Thr Val Arg Phe Ala Arg Lys Gly Ala
 260 265 270

Leu Arg Gln Lys Asn Val His Glu Val Lys Asn His Lys Phe Thr Ala
 275 280 285

Arg Phe Phe Lys Gln Pro Thr Phe Cys Ser His Cys Thr Asp Phe Ile
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Trp Gly Phe Gly Lys Gln Gly Phe Gln Cys Gln Val Cys Cys Phe Val
 305 310 315 320

Val His Lys Arg Cys His Glu Phe Val Thr Phe Ser Cys Pro Gly Ala
 325 330 335

Asp Lys Gly Pro Ala Ser Asp Asp Pro Arg Ser Lys His Lys Phe Lys
 340 345 350

Ile His Thr Tyr Ser Ser Pro Thr Phe Cys Asp His Cys Gly Ser Leu
 355 360 365

Leu Tyr Gly Leu Ile His Gln Gly Met Lys Cys Asp Thr Cys Met Met
 370 375 380

Asn Val His Lys Arg Cys Val Met Asn Val Pro Ser Leu Cys Gly Thr
 385 390 395 400

Asp His Thr Glu Arg Arg Gly Arg Ile Tyr Ile Gln Ala His Ile Asp
 405 410 415

Arg Asp Val Leu Ile Val Leu Val Arg Asp Ala Lys Asn Leu Val Pro
 420 425 430

Met Asp Pro Asn Gly Leu Ser Asp Pro Tyr Val Lys Leu Lys Leu Ile
 435 440 445

Pro Asp Pro Lys Ser Glu Ser Lys Gln Lys Thr Lys Thr Ile Lys Cys
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Ser Leu Asn Pro Glu Trp Asn Glu Thr Phe Arg Phe Gln Leu Lys Glu
465 470 475 480

Ser Asp Lys Asp Arg Arg Leu Ser Val Glu Ile Trp Asp Trp Asp Leu
485 490 495

Thr Ser Arg Asn Asp Phe Met Gly Ser Leu Ser Phe Gly Ile Ser Glu
500 505 510

Leu Gln Lys Ala Ser Val Asp Gly Trp Phe Lys Leu Leu Ser Gln Glu
515 520 525

Glu Gly Glu Tyr Phe Asn Val Pro Val Pro Pro Glu Gly Ser Glu Ala
530 535 540

Asn Glu Glu Leu Arg Gln Lys Phe Glu Arg Ala Lys Ile Ser Gln Gly
545 550 555 560

Thr Lys Val Pro Glu Glu Lys Thr Thr Asn Thr Val Ser Lys Phe Asp
565 570 575

Asn Asn Gly Asn Arg Asp Arg Met Lys Leu Thr Asp Phe Asn Phe Leu
580 585 590

Met Val Leu Gly Lys Gly Ser Phe Gly Lys Val Met Leu Ser Glu Arg
595 600 605

Lys Gly Thr Asp Glu Leu Tyr Ala Val Lys Ile Leu Lys Lys Asp Val
610 615 620

Val Ile Gln Asp Asp Asp Val Glu Cys Thr Met Val Glu Lys Arg Val
625 630 635 640

Leu Ala Leu Pro Gly Lys Pro Pro Phe Leu Thr Gln Leu His Ser Cys
645 650 655

Phe Gln Thr Met Asp Arg Leu Tyr Phe Val Met Glu Tyr Val Asn Gly
660 665 670

Gly Asp Leu Met Tyr His Ile Gln Gln Val Gly Arg Phe Lys Glu Pro
675 680 685

His Ala Val Phe Tyr Ala Ala Glu Ile Ala Ile Gly Leu Phe Phe Leu
690 695 700

Gln Ser Lys Gly Ile Ile Tyr Arg Asp Leu Lys Leu Asp Asn Val Met
705 710 715 720

Leu Asp Ser Glu Gly His Ile Lys Ile Ala Asp Phe Gly Met Cys Lys
725 730 735

Glu Asn Ile Trp Asp Gly Val Thr Thr Lys Thr Phe Cys Gly Thr Pro
740 745 750

Asp Tyr Ile Ala Pro Glu Ile Ile Ala Tyr Gln Pro Tyr Gly Lys Ser
755 760 765

Val Asp Trp Trp Ala Phe Gly Val Leu Leu Tyr Glu Met Leu Ala Gly
770 775 780

Gln Ala Pro Phe Glu Gly Glu Asp Glu Asp Glu Leu Phe Gln Ser Ile
785 790 795 800

Met Glu His Asn Val Ala Tyr Pro Lys Ser Met Ser Lys Glu Ala Val
805 810 815

Ala Ile Cys Lys Gly Leu Met Thr Lys His Pro Gly Lys Arg Leu Gly
820 825 830

Cys Gly Pro Glu Gly Glu Arg Asp Ile Lys Glu His Ala Phe Phe Arg
835 840 845

Tyr Ile Asp Trp Glu Lys Leu Glu Arg Lys Glu Ile Gln Pro Pro Tyr
850 855 860

Lys Pro Lys Ala Arg Asp Lys Arg Asp Thr Ser Asn Phe Asp Lys Glu
865 870 875 880

Phe Thr Arg Gln Pro Val Glu Leu Thr Pro Thr Asp Lys Leu Phe Ile
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<210> 23
<211> 55
<212> DNA
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 <211> 55
 <212> DNA
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 <212> DNA
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<210> 29
<211> 33
<212> DNA
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24

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<211> 33
<212> DNA
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<220>
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33